



Uemura7.ST25.txt

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SEQUENCE LISTING

<110> UEMURA, Hidetoshi
OKUI, Akira
KOMINAMI, Katsuya
YAMAGUCHI, Nozomi
MITSUI, Shinichi

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<140> 09/856,371

<141> 2001-05-21

<150> JP 10/347785

<151> 1998-11-20

<150> PCT/JP99/06475

<151> 1999-11-19

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<170> PatentIn version 3.1

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Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu
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 Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser
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45 50 55

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60 65 70

Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr
75 80 85 90

Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr
95 100 105

Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly
110 115 120

Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro Ser His Thr
125 130 135

His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu Leu Ser Thr
140 145 150

His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu Thr His Arg
155 160 165 170

Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly
175 180 185

Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr Trp His Leu
190 195 200

Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro
205 210 215

Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr
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Val Gln Val Arg
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gaccctgagg ctttacaaca gtgctactga cccct atg agc ctg atg ctg gat 173

Met Ser Leu Met Leu Asp

-215

gac caa ccc cct atg gag gcc cag tat gca gag gag ggc cca gga 218

Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala Glu Glu Gly Pro Gly

-210

-205

-200

cct ggg atc ttc aga gca gag cct gga gac cag cag cat ccc att 263

Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln Gln His Pro Ile

-195

-190

-185

tct cag gcg gtg tgc tgg cgt tcc atg cga cgt ggc tgt gca gtg 308

Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly Cys Ala Val

-180

-175

-170

ctg gga gcc ctg ggg ctg ctg gcc ggt gca ggt gtt ggc tca tgg 353

Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly Ser Trp

-165

-160

-155

ctc cta gtg ctg tat ctg tgt cct gct gcc tct cag ccc att tcc 398

Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile Ser

-150

-145

-140

ggg acc ttg cag gat gag gag ata act ttg agc tgc tca gag gcc 443

Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala

-135

-130

-125

agc gct gag gaa gct ctg ctc cct gca ctc ccc aaa aca gta tct 488

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser

-120

-115

-110

ttc aga ata aac agc gaa gac ttc ttg ctg gaa gcg caa gtg agg gat 536

Phe Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp

-105

-100

-95

cag cca cgc tgg ctc ctg gtc tgc cat gag ggc tgg agc ccc gcc ctg 584

Gln Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu

-90

-85

-80

-75

ggg ctg cag atc tgc tgg agc ctt ggg cat ctc aga ctc act cac cac 632

Gly Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His

-70

-65

-60

aag gga gta aac ctc act gac atc aaa ctc aac agt tcc cag gag ttt 680

Lys Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe

-55

-50

-45

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Ala Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln

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ccc agg aac aac tgc act tct ggt caa gtt gtt tcc ctc aga tgc tct Pro Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser -25 -20 -15			776
gag tgt gga gcg agg ccc ctg gct tcc cgg ata gtt ggt ggg cag tct Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser -10 -5 -1 1 5			824
gtg gct cct ggg cgc tgg ccg tgg cag gcc agc gtg gcc ctg ggc ttc Val Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe 10 15 20			872
cgg cac acg tgt ggg ggc tct gtg cta gcg cca cgc tgg gtg gtg act Arg His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr 25 30 35			920
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ggg gct ctg gtg gag agg att atc cca cac ccc ctc tac agt gcc cag Gly Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln 75 80 85			1064
aat cat gac tac gac gtc gcc ctc ctg agg ctc cag acc gct ctc aac Asn His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn 90 95 100			1112
ttc tca gac act gtg ggc gct gtg tgc ctg ccg gcc aag gaa cag cat Phe Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His 105 110 115			1160
ttt ccg aag ggc tcg cgg tgc tgg gtg tct ggc tgg ggc cac acc cac Phe Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His 120 125 130			1208
cct agc cat act tac agc tcg gat atg ctc cag gac acg gtg gtg ccc Pro Ser His Thr Tyr Ser Ser Asp Met Leu Gln Asp Thr Val Val Pro 135 140 145 150			1256
ttg ttc agc act cag ctc tgc aac agc tct tgc gtg tac agc gga gcc Leu Phe Ser Thr Gln Leu Cys Asn Ser Ser Cys Val Tyr Ser Gly Ala 155 160 165			1304
ctc acc ccc cgc atg ctt tgc gct ggc tac ctg gac gga agg gct gat Leu Thr Pro Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp 170 175 180			1352
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ccc aat cac cca ggt gtc tac gcc aag gta gct gag ttt ctg gac tgg			1496

Pro Asn His Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp
 215 220 225 230
 atc cat gac act gct cag gac tcc ctc ctc tgagtcctgc tgtttcctcc 1546
 Ile His Asp Thr Ala Gln Asp Ser Leu Leu
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<210> 10
 <211> 457
 <212> PRT
 <213> Homo sapiens
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 -200 -195 -190
 Asp Gln Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met
 -185 -180 -175
 Arg Arg Gly Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly
 -170 -165 -160
 Ala Gly Val Gly Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala
 -155 -150 -145
 Ala Ser Gln Pro Ile Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr
 -140 -135 -130

Leu Ser Cys Ser Glu Ala Ser Ala Glu Glu Ala Leu Leu Pro Ala
 -125 -120 -115
 Leu Pro Lys Thr Val Ser Phe Arg Ile Asn Ser Glu Asp Phe Leu
 -110 -105 -100
 Leu Glu Ala Gln Val Arg Asp Gln Pro Arg Trp Leu Leu Val Cys His
 -95 -90 -85
 Glu Gly Trp Ser Pro Ala Leu Gly Leu Gln Ile Cys Trp Ser Leu Gly
 -80 -75 -70
 His Leu Arg Leu Thr His His Lys Gly Val Asn Leu Thr Asp Ile Lys
 -65 -60 -55 -50
 Leu Asn Ser Ser Gln Glu Phe Ala Gln Leu Ser Pro Arg Leu Gly Gly
 -45 -40 -35
 Phe Leu Glu Glu Ala Trp Gln Pro Arg Asn Asn Cys Thr Ser Gly Gln
 -30 -25 -20
 Val Val Ser Leu Arg Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser
 -15 -10 -5
 Arg Ile Val Gly Gly Gln Ser Val Ala Pro Gly Arg Trp Pro Trp Gln
 -1 1 5 10 15
 Ala Ser Val Ala Leu Gly Phe Arg His Thr Cys Gly Gly Ser Val Leu
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 Ala Pro Arg Trp Val Val Thr Ala Ala His Cys Met His Ser Phe Arg
 35 40 45
 Leu Ala Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His
 50 55 60
 Ser Ala Val Arg Pro His Gln Gly Ala Leu Val Glu Arg Ile Ile Pro
 65 70 75
 His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu
 80 85 90 95
 Arg Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val Cys
 100 105 110
 Leu Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp Val
 115 120 125

Ser Gly Trp Gly His Thr His Pro Ser His Thr Tyr Ser Ser Asp Met
 130 135 140

Leu Gln Asp Thr Val Val Pro Leu Phe Ser Thr Gln Leu Cys Asn Ser
 145 150 155

Ser Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala Gly
 160 165 170 175

Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro
 180 185 190

Leu Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val Ser
 195 200 205

Trp Gly Arg Ala Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala Lys
 210 215 220

Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Asp Ser Leu
 225 230 235

Leu
 240

<210> 11
 <211> 99
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<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <223> Designed oligonucleotide to construct plasmid pSecTrypHis

<400> 11
 aagcttggtgct agcaacacca tgaatctact cctgatacctt acctttgttg ctgctgctgt 60
 tgctgcccc tttgacgacg atgacaagga tccgaattc 99

<210> 12
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
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 <223> Designed oligonucleotide to construct plasmid pSecTrypHis

<400> 12
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 aggatcagga gtagattcat ggtgttgcta gccaaagctt 99

<210> 13
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <223> Designed oligonucleotide primer t amplify neurosin-encoding sequence

<400> 13
 ttggtgcatg gcgga 15

<210> 14
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

<400> 14
 tcctcgagac ttggcctgaa tggtttt 27

<210> 15
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p SecTrypHis/Neurosin

<400> 15
 gcgctagcag atctccatga atctactcct gatcc 35

<210> 16

<211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <220>
 <221> misc_feature
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p
 SecTrypHis/Neurosin

 <400> 16
 tgaagcttgc catggaccaa cttgtcatc 29

 <210> 17
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <220>
 <221> misc_feature
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p
 TrypHis

 <400> 17
 ocaagcttca ccatcaccat caccat 26

 <210> 18
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <220>
 <221> misc_feature
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p
 TrypSigTag

 <400> 18
 gcacagtcga ggctgat 17

 <210> 19
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <220>
 <221> misc_feature

<223> Designed oligonucleotide primer to amplify a portion of plasmid p
FBTrypSigTag

<400> 19
caaattgtggt atggctg

17

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
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<223> Designed oligonucleotide primer to amplify conserved region of se
rin proteases-encoding sequence

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g or t.

<220>
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<222> (12)..(12)
<223> n is a, c, g or t.

<400> 20
gtgctcacng cngcbcaytg

20

<210> 21
<211> 20
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<220>
<223> Synthetic

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rin proteases-encoding sequence

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<400> 21
ccvctrwsdc cncnggcga 20

<210> 22
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<220>
<223> Synthetic

<220>
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<223> Designed oligonucleotide primer designated as mBSSP2.0 for RACE f
or mBSSP2 (forward)

<400> 22
atggtggaga agatcattcc t 21

<210> 23
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
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or mBSSP2 (forward)

<400> 23
tacagtgcc agaaccatg 19

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
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r mBSSP2 (forward)

<400> 24
ctcaactctc tgctagaccg 20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic

<220>
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 <223> Designed oligonucleotide primer designated as mBSSP2F5 to amplify
 mature mBSSP2-encoding region (forward)

<400> 25
 atagttggcg gccaaagctgt 20

<210> 26
 <211> 20
 <212> DNA
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<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <223> Designed oligonucleotide primer designated as mBSSP2.2 for RACE f
 or mBSSP2 (reverse)

<400> 26
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<210> 27
 <211> 20
 <212> DNA
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<220>
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<220>
 <221> misc_feature
 <223> Designed oligonucleotide primer designated as mBSSP2E2 for RACE f
 or mBSSP2 (reverse)

<400> 27
 tgttgcagag gtgggtgctg 20

<210> 28
 <211> 21
 <212> DNA
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<220>
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<220>
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 <223> Designed oligonucleotide primer designated as mBSSP2R2 for RACE f
 or mBSSP2 (reverse)

<400> 28
taccattgtg tcctgcagtg t 21

<210> 29
<211> 27
<212> DNA
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<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as mBSSP2R5/E to amplify full-length mBSSP2-encoding mRNA (reverse)

<400> 29
tgaattctgc tgcttcttcg gctagcg 27

<210> 30
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as BSSP2SPF to amplify a portion of hBSSP2 (forward)

<400> 30
actgctgccc actgcatg 18

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as BSSP2SPR to amplify a portion of hBSSP2 (reverse)

<400> 31
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<210> 32
<211> 20
<212> DNA
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<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <223> Designed oligonucleotide primer designated as hBSSP2F11 for RACE
 for hBSSP2 (forward)

<400> 32
 gctctcaact tctcagacac 20

<210> 33
 <211> 20
 <212> DNA
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<220>
 <223> Synthetic

<220>
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 <223> Designed oligonucleotide primer designated as hBSSP2R12 for RACE
 for hBSSP2 (reverse)

<400> 33
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<210> 34
 <211> 20
 <212> DNA
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<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <223> Designed oligonucleotide primer designated as hBSSP2R11 for RACE
 for hBSSP2 (reverse)

<400> 34
 cctggagcat atccgagctg 20

<210> 35
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
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<220>
 <221> misc_feature
 <223> Designed oligonucleotide primer designated as hBSSP2F12 to amplif
 y full length hBSSP2 (forward)

<400> 35
gctttacaac agtgctac 18

<210> 36
<211> 28
<212> DNA
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<220>
<223> Synthetic

<220>
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<223> Designed oligonucleotide primer designated as hBSSP2R13/E to amplify full length hBSSP2 (reverse)

<400> 36
tggaattcga ggaaacagca ggactcag 28

<210> 37
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<220>
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<223> Designed oligonucleotide primer for RACE for hBSSP2

<400> 37
tactagtcga cgcgtggcc 19

<210> 38
<211> 18
<212> DNA
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<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as hBSSP2F13 to amplify a portion of hBSSP2 (forward)

<400> 38
actgctgccc actgcatg 18

<210> 39
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <223> Designed oligonucleotide primer designated as FBTrpsigtagF5 to de
 tect hBSSP2

<400> 39
 ggcgctagcag atctccatga atctactcct gatcc 35

<210> 40
 <211> 117
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 40
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<210> 41
 <211> 117
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<220>
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<220>
 <221> misc_feature
 <223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 41
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<210> 42
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 42
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 1 5

<210> 43
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 43

Leu Val His Gly
 1

<210> 44
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 44
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37

Φ'
 Corel.